

Run on: April 30, 2002, 19:51:03 ; Search time 2499.58 seconds
(without alignments)
11483.966 Million cell updates/sec

Title: US-09-668-119-1
Perfect score: 1740
Sequence: 1 atgaggaagctgtgtgtgc.....cacatcgttcagcagcatga 1740

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

*Searched: 1472140 seqs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2944280

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Listing first 45 summaries

Database

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3:  gb_in.*
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10: gb_ro.*
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12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_om.*
20: em_ov.*
21: em_ov.*
22: em_pat.*
23: em_ph.*
24: em_pl.*
25: em_ro.*
26: em_sts.*
27: em_sy.*
28: em_un.*
29: em_vl.*
30: em_hgt_hum.*
31: em_hgt_inv.*
32: em_hgt_rod.*
33: em_hgt_hum.*
34: em_hgt_inv.*
35: em_hgt_rod.*
36: em_hgt_other.*

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RESULT	12		
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LOCUS	AF021108	236 bp	DNA
DEFINITION	Homo sapiens trinucleotide repeat CTG-13, sequence tagged site.		
ACCESSION	AF021108		
VERSION	AF021108.1	GI:3015581	
KEYWORDS	STS.		
SOURCE	human.		

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 236)
Philliber, R. A., Horelli-Kultunen, N., Robb, A. S., Lee, Y. H.,
REFERENCE
AUTHORS

TITLE

JOURNAL	Eur. J. Hum. Genet. 6 (1), 89-94 (1998)
MEDLINE	98454304
REFERENCE	2 (bases 1 to 236)
AUTHORS	Philibert, R.A., Horelli-Kuitunen, N., Ro

TITLE
Direct Submission
JOURNAL Submitted (28-AUG-1997) Clinical Neuroscience Branch, National

FEATURES

Institutes of Mental Health, 49 Convent Drive Rm B1EE16, Bethesda, MD 20892, USA	
Location/Qualifiers	

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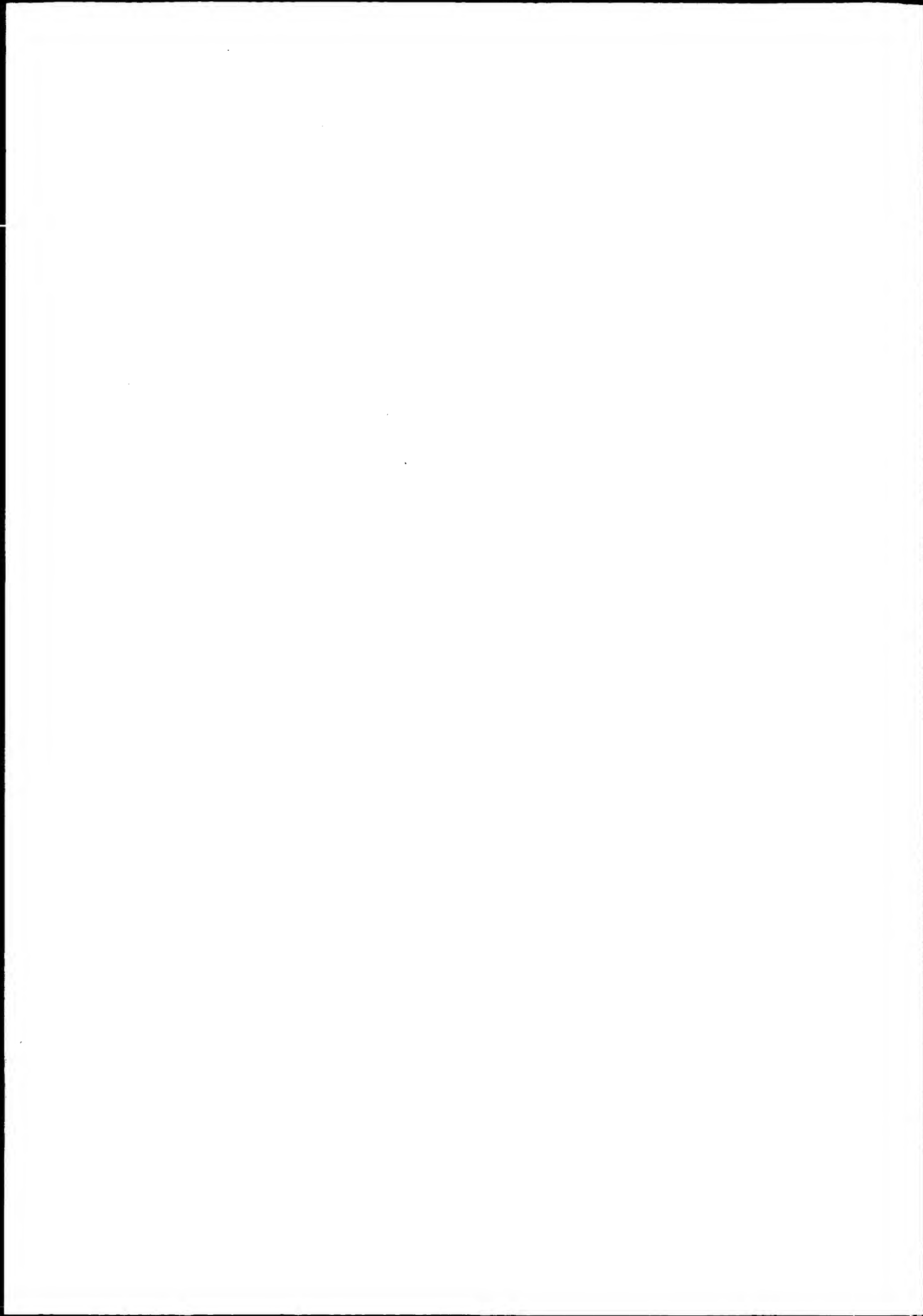
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/db_xref="taxon:9606"
/chromosome="22"
/note="primers to amplify repeat: forward:
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ORIGIN

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Matches 86; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0

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Db	86	AAGCAGTGTGCACGAGCAGCAGCTCCACGACGACGACGACAGCATCTTA	27
Qy	584	ttaaatgtcatcatcaaaaatcaggcaa	609
Db	26	TTTAAATTCATCATCAAAATGAGCAA	1

File copy



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2002, 19:51:03 ; Search time 2499.58 Seconds
(without alignments)
11483.966 Million cell updates/sec

Title: US-09-668-119-1

Perfect score: 1740
Sequence: 1 atgaggaagaagctgtgtgc.....cacatctctccagccatga 1740

Scoring table:
OLIGO_NUC
Gapex 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
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3: gb.in:*
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8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.om:*
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26: em.sts:*
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29: em.vi:*
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31: em.htgo.in:*
32: em.htgo.ro:*
33: em.htgo.hum:*
34: em.htg.in:*
35: em.htg.ro:*
36: em.htg.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1740	100.0	3334	9	AF056191	AF056191 Homo sapi
2	1092	62.8	3170	9	AF328769	AF328769 Homo sapi
3	962	55.3	1048	9	HS080745	HS080745 Homo sapi
4	549	31.6	2106	9	BC007529	BC007529 Homo sapi
5	304	17.5	64231	2	AL359452	AL359452 Homo sapi
6	304	17.5	157080	2	AL358856	AL358856 Homo sapi
7	304	17.5	163908	9	AC007030	AC007030 Homo sapi
8	250	14.4	145356	9	AC004033	AC004033 Homo sapi
9	203	11.7	4701	2	AK000003	AK000003 Homo sapi
10	137	7.9	64231	2	AL359452	AL359452 Homo sapi
11	132	7.6	386	6	AX071270	AX071270 Sequence
12	86	4.9	236	11	AF021108	AF021108 Homo sapi
13	79	4.5	192592	9	AC005500	AC005500 Homo sapi
14	48	2.8	107642	10	AF125313	AF125313 Mus muscu
15	45	2.6	164	11	PCU64652	PCU64652 Paracharter
16	45	2.6	307	11	G64292	G64292 6 Human Hom
17	45	2.6	383	9	HSORP1A	HSORP1A H. sapiens O
18	45	2.6	632	9	AF223572	AF223572 Homo sapi
19	45	2.6	920	9	HSTFLIDBA	HSTFLIDBA H. sapiens L
20	45	2.6	942	9	PPA133270	PPA133270 Pan panis
21	45	2.6	1020	9	HUMTFE1IDA	HUMTFE1IDA Homo sapien
22	45	2.6	1310	6	AX002276	AX002276 Sequence
23	45	2.6	1310	6	E28256	E28256 Purificatio
24	45	2.6	1475	9	HUMRNF	HUMRNF Human (clon
25	45	2.6	1710	9	HSTFLIDX	HSTFLIDX H. sapiens.T
26	45	2.6	1876	9	HUMTFE1ID	HUMTFE1ID Human TATA-
27	45	2.6	3263	6	AX002278	AX002278 Sequence
28	45	2.6	4286	6	E28258	E28258 Purificatio
29	45	2.6	4286	6	AX002277	AX002277 Sequence
30	45	2.6	4286	6	E28257	E28257 Purificatio
31	45	2.6	113820	9	HS191N21	HS191N21 Human DNA
32	45	2.6	157115	9	AC006512	AC006512 Homo sapi
33	45	2.6	171288	2	AC019343	AC019343 Homo sapi
34	45	2.6	179289	2	AC024883	AC024883 Mus muscu
35	45	2.6	222930	9	HSU47924	HSU47924 Human chrom
36	44	2.5	1654	10	MMPOU2	MMPOU2 M. musculus
37	44	2.5	3200	10	RATARB	RATARB Rat androge
38	44	2.5	3217	6	IO9480	IO9480 Sequence 2
39	44	2.5	3864	10	MUSPOUDOMB	MUSPOUDOMB Mouse brain
40	44	2.5	4135	6	IO9511	IO9511 Sequence 3
41	44	2.5	4137	10	RATANDREC	RATANDREC Rat androge
42	44	2.5	202807	10	AC021063	AC021063 Mus Muscu
43	43	2.5	3166	3	DROENGA	DROENGA D. virilis e
44	43	2.5	217616	2	AC079531	AC079531 Mus muscu
45	42	2.4	163	4	BOVTBPR	BOVTBPR Bos taurus

ALIGNMENTS

RESULT 1	AF056191	3334 bp	mRNA	PRI	11-OCT-2000
LOCUS	AF056191				
DEFINITION	Homo sapiens TPA Inducible protein mRNA, complete cds.				
ACCESSION	AF056191				
VERSION	AF056191.1	GI:3037134			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1	(bases 1 to 3334)			
AUTHORS	Abraham, S. and Solomon, W.B.				
TITLE	A novel glutamine-rich putative transcriptional adaptor protein (TIG-1), preferentially expressed in placental and bone-marrow tissues				
JOURNAL	Gene 255 (2), 389-400 (2000)				
PubMed	11024300				
REFERENCE	2	(bases 1 to 3334)			
AUTHORS	Abraham, S. and Solomon, W.B.				


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ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL      1 (bases 1 to 145356)
REFERENCE     Budarf, M.L. and Emanuel, B.S.
JOURNAL      Unpublished
AUTHORS      2 (bases 1 to 145356)
JOURNAL      Zhang, G., Lao, V., Zhan, M., and Roe, B.A.
REFERENCE     Homo sapiens Chromosome 22q11.2 BAC Clone p.m11 In BCR12-GGT Region
JOURNAL      Unpublished
AUTHORS      3 (bases 1 to 145356)
JOURNAL      Zhang, G., Lao, V., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
REFERENCE     Direct Submission
AUTHORS      4 (bases 1 to 145356)
JOURNAL      Submitted (26-JAN-1998) Department Of Chemistry And Biochemistry,
JOURNAL      The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
JOURNAL      OK 73019, USA
REFERENCE     5 (bases 1 to 145356)
JOURNAL      Zhang, G., Lao, V., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
REFERENCE     Direct Submission
AUTHORS      Submitted (09-DEC-1998) Department Of Chemistry And Biochemistry,
JOURNAL      The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
JOURNAL      OK 73019, USA
REFERENCE     6 (bases 1 to 145356)
JOURNAL      Zhang, G., Lao, V., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
REFERENCE     Direct Submission
AUTHORS      Submitted (04-FEB-1999) Department Of Chemistry And Biochemistry,
JOURNAL      The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
JOURNAL      OK 73019, USA
REFERENCE     7 (bases 1 to 145356)
JOURNAL      Zhang, G., Lao, V., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
REFERENCE     Direct Submission
AUTHORS      Submitted (09-APR-1999) Department Of Chemistry And Biochemistry,
JOURNAL      The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
JOURNAL      OK 73019, USA
REFERENCE     8 (bases 1 to 145356)
JOURNAL      Zhang, G., Lao, V., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
REFERENCE     Direct Submission
AUTHORS      Submitted (12-APR-1999) Department Of Chemistry And Biochemistry,
JOURNAL      The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
JOURNAL      OK 73019, USA
REFERENCE     9 (bases 1 to 145356)
JOURNAL      Zhang, G., Lao, V., Zhan, M., Budarf, M.L., Emanuel, B.S. and Roe, B.A.
REFERENCE     Direct Submission
AUTHORS      Submitted (31-MAY-2000) Department Of Chemistry And Biochemistry,
JOURNAL      The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
JOURNAL      OK 73019, USA
COMMENT      On Apr 12, 1999 this sequence version replaced gi:4580479.
      Because these overlapping clones came from different libraries
      there are numerous instances of insertions, deletions, and single
      nucleotide polymorphisms in the overlapping regions below.
      AC005500(p52f6) 112352 192592 (4) overlaps AC004033(p.m11) 1 78509
      (66847) AC004033(p.m11) 89227 145356 (4) overlaps AC007050(bac32) 1
      59304 (104604).
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                        /chromosome="22"
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Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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      |||||||
Db 103886 AGGCCAGCCACCAATTCAGCAGCCAGATGCACACAGCAGCAGCCTCCGCCACAGC 103945
QY 776 cctgtccacgacgtcgtcagatgacacacacacacacacacacacacacacac 835
      |||||||
Db 103946 CTCTGCCCCAGCAGCAGCAGCAGATGCATCAGCAGCAGCAGCAGCAGCAGC 104005
QY 836 ccacgacgacccacgtgtcgtcagacacacacacacacacacacacacacacac 895
      |||||||
Db 104006 CCACGACGACCTCCAGTGTCTCAGAACACATCAGCAGCAGCAGCAGCAGCAGC 104065
QY 896 agccttggtgtcagcagcagcagcctccctggagcaatgtgtatccacacacac 955
      |||||||
Db 104066 AGCTTTGTGTGTACAGGCGCAAGCTCTCCAGCAATGTGTATACCAACACAC 104125
QY 956 tgaatttgt 965
      |||||||
Db 104126 TGAATTGTGT 104135

RESULT 9
AK000003
LOCUS      Homo sapiens mRNA for FLJ00003 protein, partial cds.
DEFINITION AK000003.1 GI:7209306
ACCESSION AK000003
VERSION    FLJ00003 protein; fls (full insert sequence).
KEYWORDS   Homo sapiens adult spleen cDNA to mRNA, clone:as00003.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL    1 (bases 1 to 4701)
JOURNAL    The nucleotide sequence of a long cDNA clone isolated from human
JOURNAL    spleen
JOURNAL    Published only in Database (2000) In press
REFERENCE 2 (bases 1 to 4701)
AUTHORS   Ohara, O., Kikuno, R., Nagase, T. and Okumura, K.
JOURNAL   Direct Submission
JOURNAL   Submitted (14-FEB-2000) to the DDBJ/EMBL/GenBank databases. Osamu
JOURNAL   Ohara, Kazusa DNA Research Institute, Department of Human Gene
JOURNAL   Research; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
JOURNAL   (E-mail:cdnaif@kazusa.or.jp, URL:http://www.kazusa.or.jp,
JOURNAL   Tel:81-438-52-3913, Fax:81-438-52-3914)
JOURNAL   NEDO human cDNA sequencing project supported by Ministry of
JOURNAL   International Trade and Industry of Japan; cDNA full insert
JOURNAL   sequencing; Research Association for Biotechnology; cDNA library
JOURNAL   construction, 5'- & 3'-end one pass sequencing and clone selection;
JOURNAL   Kazusa DNA Research Institute.
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					Gaps 0
QY	629	agcagcgcgcagcgaatatagcacagctcgcagcttccaacaacagcaacagcagcagcagc	688		

RESULT	13
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DEFINITION	Homo sapiens 22q11 PAC Clone Clone p52t6 In DGR Region, compl sequence.
ACCESSION	AC005500

VERSION AC005500.2 31:7798766
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Homo sapiens Chromosome 22q11 PAC Clone p52f6 In DGC Region
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (20-AUG-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 3 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 4 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (23-SEP-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 5 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 6 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 7 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 8 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 9 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (30-OCT-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 10 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (03-NOV-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 11 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (21-NOV-1998) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 12 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission

JOURNAL Submitted (13-MAY-2000) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 REFERENCE 13 (bases 1 to 192592)
 AUTHORS Chen, F., D.L., Do, T., Dumanski, J.P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAY-2000) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 COMMENT On May 13, 2000 this sequence version replaced gi:3900817.
 Because these overlapping clones came from different libraries
 there are numerous instances of insertions, deletions, and single
 nucleotide polymorphisms in the overlapping regions below.
 AC00773(b562f10) 5026 182617 (0) overlaps AC005500(p52f6) 1 17755
 (15037) AC005500(p52f6) 112352 192592 (0) overlaps AC004033(p_m11)
 1 78509 (66847).
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 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 188530 ATGAGGAAGCTGTGTGGCAGACAGTAATCCAGCAGGATATGGAGACCATGTTTC 188589
 Oy 61 ctgaagcgaagcccg 79
 ||||||||||||||||
 Db 188590 CTGAAGCCAGACCCG 188608
 RESULT 14
 AF125313 107642 bp DNA ROD 22-MAR-2000
 LOCUS Mus musculus x chromosome: Cg1/Xap80 gene, complete sequence.
 DEFINITION AF125313
 ACCESSION AF125313.1 GI:6650998
 VERSION HTG.
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 107642)
 AUTHORS Platzer, M., Zhao, W., Herman, G.E. and Rosenthal, A.
 TITLE Comparative sequence analysis of the mouse Mtm locus and the
 corresponding region of human Xq28
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 107642)
 AUTHORS Platzer, M.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-1999) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
 COMMENT This sequence is part of a larger genomic contig. The start of this
 sequence is directed towards the centromere. The end
 (107933..107642) of this sequence overlaps with the start of the
 neighboring sequence deposited in Genbank Accession Number
 AF125314.
 FEATURES
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 /db_xref="taxon:10090"
 /chromosome="X"
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repeat_region	complement(1452..1611)	repeat_region	/rpt_family="POLY_A"
repeat_region	/rpt_family="L1MC4"	repeat_region	15218..15552
repeat_region	1789..2073	repeat_region	/rpt_family="MIR1C"
repeat_region	/rpt_family="MIR1A1"	repeat_region	complement(15570..15798)
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repeat_region	/rpt_family="L1MC4"	repeat_region	complement(15898..16075)
repeat_region	complement(3067..3238)	repeat_region	/rpt_family="L1M2"
repeat_region	/rpt_family="L1MD3"	repeat_region	complement(16410..16698)
repeat_region	complement(3475..3580)	repeat_region	/rpt_family="L1M1"
repeat_region	/rpt_family="L1MC4"	repeat_region	complement(17963..18084)
repeat_region	complement(3668..3720)	repeat_region	/rpt_family="MIR"
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repeat_region	/rpt_family="L1ME"	repeat_region	complement(19936..20069)
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repeat_region	/rpt_family="AT_rich"	repeat_region	complement(21355..21462)
repeat_region	complement(4653..4710)	repeat_region	/rpt_family="(CA)n"
repeat_region	/rpt_family="B4"	repeat_region	complement(21475..21592)
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repeat_region	/rpt_family="A-rich"	repeat_region	complement(22549..22708)
repeat_region	complement(5212..5684)	repeat_region	/rpt_family="MIR"
repeat_region	/rpt_family="L1M4"	repeat_region	complement(22835..22933)
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repeat_region	complement(6012..6168)	repeat_region	/rpt_family="B1_MM"
repeat_region	/rpt_family="L1M4"	repeat_region	complement(23761..23848)
repeat_region	complement(6189..6305)	repeat_region	/rpt_family="B4A"
repeat_region	/rpt_family="L1MA9"	repeat_region	complement(25114..25177)
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repeat_region	complement(6730..6884)	repeat_region	/rpt_family="(CA)n"
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repeat_region	/rpt_family="B4A"	repeat_region	31294..31517
repeat_region	complement(8501..8860)	repeat_region	/rpt_family="Lx9"
repeat_region	/rpt_family="L1M4"	repeat_region	31518..31780
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repeat_region	/rpt_family="Lx8"	repeat_region	complement(32109..32186)
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repeat_region	/rpt_family="L1MC1"	repeat_region	complement(32470..32548)
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repeat_region	complement(11655..12179)	repeat_region	/rpt_family="URR1B"
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repeat_region	/rpt_family="L1MB2"	repeat_region	complement(34371..34548)

Wed May 1 16:36:04 2002

us-09-668-119-1.oli.rge

Page 15

1. 1. 1.

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2002, 19:49:19 ; Search time 182.29 Seconds

(without alignments)
8183.367 Million cell updates/sec

Title: US-09-668-119-1
Perfect score: 1740
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Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 4: /SIDSI/gcgdata/geneseq/geneseq/NA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1518	87.2	2556	22	AA159455 Human polynucleoti
2	848	48.7	3458	22	AA161241 Human polynucleoti
3	777	44.7	1388	21	AA159039 Human polynucleoti
4	239	13.7	316	22	AA120017 Probe #9950 for ge
5	239	13.7	316	22	AA145215 Probe #13901 used
6	239	13.7	316	22	AA105725 Probe #5716 used t
7	239	13.7	436	22	AA110775 Probe #7108 for gen
8	239	13.7	436	22	AA132033 Probe #719 used to
9	239	13.7	436	22	AA100701 Probe #692 used to
10	132	7.6	386	22	AA165986 Novel human polynu
11	73	4.2	232	21	AA109371 Human secreted pro

12	45	2.6	203	19	AAV30271
13	45	2.6	203	19	AAV17226
14	45	2.6	1310	20	AAV08558
15	45	2.6	3263	20	AAV08560
16	45	2.6	4286	20	AAV08559
17	44	2.5	3217	10	AAV91578
18	44	2.5	3217	12	AAQ12002
19	44	2.5	4180	10	AAV91773
20	42	2.4	293	22	AAI21460
21	42	2.4	293	22	AAI46749
22	42	2.4	293	22	AAI07156
23	42	2.4	397	20	AAV89891
24	42	2.4	459	22	AAI12263
25	42	2.4	459	22	AAI33617
26	42	2.4	459	22	AAI02177
27	42	2.4	1776	20	AAZ23425
28	42	2.4	2415	18	AAI6757
29	42	2.4	2453	18	AAI6758
30	41	2.4	1853	19	AAV06751
31	41	2.4	4279	20	AAZ23430
32	41	2.4	4789	20	AAV80992
33	40	2.3	107	21	AAI18151
34	39	2.2	2171	21	AAV35075
35	39	2.2	2224	19	AAV35472
36	39	2.2	2733	20	AAV84442
37	39	2.2	8564	21	AAI4783
38	38	2.2	102	22	AAI24904
39	38	2.2	102	22	AAI50516
40	38	2.2	374	22	AAI66719
41	38	2.2	491	22	AAI15681
42	38	2.2	491	22	AAI37333
43	38	2.2	1635	21	AAI62682
44	38	2.2	2333	22	AAI75339
45	38	2.2	3302	22	AAI58388

ALIGNMENTS

RESULT 1	
AA159455	AA159455 standard; cDNA; 2556 BP.
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AC	AA159455;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 1658.
XX	
KW	Human; nootropic; immunosuppressant; cytosolic; gene therapy; cancer;
KW	peripheral nervous system; neuropathy; central nervous system; CNS;
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW	leukaemia; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200153312-A1.
XX	
PD	26-JUL-2001.
XX	
PF	26-DEC-2000; 2000WO-US34263.
XX	
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0695036.
PR	29-NOV-2000; 2000US-0727344.
XX	

Glutamine rich reg
SCA2 gene CAG repe
Transgene for epit
Transgene for epit
Rat androgen recep
Full-length rat an
Rat androgen recep
Probe #11393 for g
Probe #15435 used
Probe #7147 used t
Sphincerebellar at
Probe #2196 for ge
Probe #2303 used t
Probe #2168 used t
Human Machado-Jose
CDNA of the M3/6 g
CDNA of the M3/6 g
Dentatorubral-pall
Human atrophin I D
Human steroid rece
Human secreted pro
Human secreted pro
Rat RSK3 coding se
Mouse brain CNG-1
Human OREF3 ORF38
Probe #14837 for g
Probe #19202 used
Novel human polynu
Probe #5614 for ge
Probe #6019 used t
Human ASH1 gene.
Human TGF-beta rec
Human polynucleoti

[illegible]

1
2
3
4

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2002, 16:38:07 ; Search time 1518.73 Seconds
(without alignments)
12311.375 Million cell updates/sec

Title: US-09-668-119-1
Perfect score: 1740
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Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :
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1: em_estfun:
2: em_esthum:
3: em_estin:
4: em_estom:
5: em_estipl:
6: em_estiba:
7: em_estiro:
8: em_estrov:
9: em_hic:
10: gb_estl:
11: gb_est2:
12: gb_hic:
13: gb_gss:
14: em_gss_fun:
15: em_gss_hum:
16: em_gss_in:
17: em_gss_pln:
18: em_gss_pro:
19: em_gss_rnd:
20: em_gss_vit:
21: em_gss_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	32.5	730	11	BG766214 602737942
2	551	31.7	2752	12	BC005027 Homo sapi
3	509	29.3	620	10	BE384305 601272684
4	475	27.3	526	10	BE019568 ba83f05.y
5	450	25.9	776	11	BG750043 602708813
6	431	24.8	482	10	AA664125 ac06c04.s
7	418	24.0	914	11	BG468341 602509947
8	399	22.9	756	11	BG746380 602703648
9	395	22.7	886	11	BG281923 602403104
10	385	22.1	723	10	BE279307 601157640
11	357	20.5	486	10	AW747905 QV1-BN000
12	347	19.9	757	10	AL046886 DKFZ586E

C	13	340	19.5	501	10	BE163519	BE163519 QV3-HT046
	14	327	18.8	976	11	BG122694	BG122694 602351822
	15	319	18.3	858	11	BG386117	BG386117 602455292
C	16	308	17.7	524	10	BE410770	BE410770 601301681
	17	301	17.3	498	10	AM603679	AM603679 CM0-CN003
	18	292	16.8	656	10	BE390284	BE390284 601285167
	19	287	16.5	557	11	BG421332	BG421332 602451441
	20	283	16.3	1019	11	BG352275	BG352275 602403789
	21	267	15.3	424	10	AM501171	AM501171 UI-HF-BP0
	22	267	15.3	428	11	BE889171	BE889171 601513434
	23	260	14.9	386	11	BG982754	BG982754 PM0-CN015
	24	255	14.7	1157	11	BG177319	BG177319 602313922
	25	254	14.6	393	10	AM499614	AM499614 UI-HF-BP0
	26	252	14.5	391	10	AM500833	AM500833 UI-HF-BP0
	27	242	13.9	313	11	NA9344	NA9344 y23e10.r1
	28	241	13.9	386	11	BG982761	BG982761 PM0-CN015
	29	236	13.6	434	11	BF346622	BF346622 602021224
	30	216	12.4	942	11	BG338685	BG338685 602436442
C	31	211	12.1	335	11	B1011820	B1011820 PM1-EN006
	32	185	10.6	939	11	BG336790	BG336790 602405533
	33	181	10.4	235	11	BF994170	BF994170 CM2-GN016
	34	172	9.9	733	10	BE391135	BE391135 601286095
	35	170	9.8	348	11	T07163	T07163 EST05052.FE
C	36	169	9.7	258	11	BF755836	BF755836 CM3-CT057
	37	164	9.4	810	11	BG686794	BG686794 602650765
	38	164	9.4	1043	11	BF974180	BF974180 602243806
C	39	158	9.1	443	11	B1024741	B1024741 PM0-WT020
	40	143	8.2	668	11	BG766083	BG766083 602738467
C	41	138	7.9	255	11	BF870481	BF870481 IL3-ET011
	42	136	7.8	568	11	B1089323	B1089323 602853282
	43	135	7.5	385	11	R17502	R17502 Y902d12.r1
C	44	130	7.5	200	11	BF084780	BF084780 IL3-CT053
	45	121	7.0	301	10	AA069235	AA069235 zml1e01.r

ALIGNMENTS

RESULT 1
LOCUS BG766214 730 bp mRNA
DEFINITION 602737942F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4862938 5', mRNA sequence.
ACCESSION BG766214
VERSION BG766214.1 GI:14076867
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
COMMENT Email: gcaps-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LCM1724 row: d column: 11
High quality sequence stop: 716.
Location/Qualifiers
1..730
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4862938"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"


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Db 481 ATCATACAACTTCCGCCACAGTCGACAGACCCAGCCTTTGGTGTCTACAGCGCCAGACTCT 540
QY 924 cccctgacaatgttatacccaaccaccactgaatttgcagagtcctcagatgtgt 983
Db 541 CCTGTGACAAATGTTATATACCAACAGCACCTGAATTTGTCGAGCTCCATGGTGT 600
QY 984 gacagacccccagtcgacccccagtcgacagcagcagcagcagcagcagcagcagcagc 1043
Db 601 GCAGCAGCCCCCAGTCGACCCAGGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 660
QY 1044 gactgccagatgtgtgtcccccagtcagagtcagagtcagagtcagagtcagagtcag 1088
Db 661 GGCTGCCAGATGTGTGCTCCGAGAGTCAGGTTCAGCCAGACAGCAG 705

RESULT 6
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LOCUS AA664125/c
DEFINITION IMAGE:655654 s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:655654 3' similar to contains element MSRI MSRI repetitive
element ;, mRNA sequence.
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VERSION AA664125.1 GI:2618116
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 482)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubnue,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Stepcoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
JOURNAL Unpublished (1997)
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 425.
Location/Qualifiers
1. 482
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:655654"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/notes="Organ: lung; Vector: pBluescript SK-; Site:1: EcoRI
; Site:2: XhoI; Cloned unidirectionally. Primer: oligo
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector: ~5' adaptor sequence: 5' GAATTCGGGACAG 3' ~3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"
BASE COUNT 51 a 113 c 176 g 142 t
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Query Match 24.8%; Score 431; DB 10; Length 482;
Best Local Similarity 99.8%; Pred. No. 3.1e-187;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 428 tccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 487
Db 482 TCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 423
QY 488 tccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 547
|||||

Db 422 TCACGAGCTCAGCAGAGTGCATGACAGCAGCAGCTTCAAGCAGTAGAGCAGCAGCAGC 363
QY 548 agcttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 607
Db 362 AGCTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 303
QY 608 aacagatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 667
Db 302 AACCATATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 243
QY 668 agcaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 727
Db 242 AGCAACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 183
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Db 182 CAATTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 123
QY 788 agcttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 847
Db 122 AGCTTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 63
QY 848 cagctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 907
Db 62 CAGTGTCTCAGACCAACCATCACAACCTCCGCCAGTTCGAGACCCAGCCTTGGTGT 3
QY 908 ca 909
Db 2 CA 1

RESULT 7
LOCUS BG468341 914 bp mRNA EST 21-MAR-2001
DEFINITION 602509947P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:464239 5',
mRNA sequence.
ACCESSION BG468341
VERSION BG468341.1 GI:13400611
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9qab8-remail.nih.gov
Tissue Procurement: ATCC
cDNA library preparation: Ling Hong/Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: BLCM1415 row: n column: 12
High quality sequence stop: 812.
Location/Qualifiers
1. 914
FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:464239"
/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit

```

	(Stratagene)	and	Superscript II RT	(Life Technologies)
BASE COUNT	225 a	305 c	229 g	155 t
ORIGIN				

REFERENCE 1 (bases 1 to 886)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DCMD/DRP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
 Plate: LNCMI230 row: g column: 02
 High quality sequence stop: 876.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /clone_lib="NIH-MGC_20"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 234 a 299 c 231 g 122 t
 ORIGIN

Query Match 22.7%; Score 395; DB 11; Length 886;
 Best Local Similarity 100.0%; Pred. No. 1.1e-170;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 cagcgccctcttggaactcgggagatggccctacacagatgctgtgtctacgca 363
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 DB 15 CAGCCGCTCTCTGGGACCTGGGGATGGCCCTCACAGCATGCTCTGTCTACGGCA 74
 QY 364 acccaacagaccagctcagctcagcagctgagctcagcagcagcagcagcag 423
 |||||||
 DB 75 ACTCCACAGACCCAGCTGCACTCCAGAGTGCGCTGAGCAGCAGCAGCAGCAG 134
 QY 424 cagttccagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 483
 |||||||
 DB 135 CAGTTCACAGCAGCAGCAGCAGCGGGGCTACACACAGCAGCAGCAGCAGCAG 194
 QY 484 cagttccagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 543
 |||||||
 DB 195 CAGTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 254
 QY 544 cagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 603
 |||||||
 DB 255 CAGCAGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 314
 QY 604 cagcaacagatatacagcagcagcagcagcagcagcagcagcagcagcagcag 663
 |||||||
 DB 315 CAGCAACAGATACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 374
 QY 664 caacaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 698
 |||||||
 DB 375 CAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 409

RESULT 10
 BE279307 723 bp mRNA EST 13-JUL-2000
 LOCUS 601157640F1 NIH_MGC_21 homo sapiens cDNA clone IMAGE:3504608 5',
 DEFINITION mRNA sequence.
 ACCESSION BE279307

VERSION BE279307.1 GI:9154297
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 723)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
 Plate: LNCMI79 row: o column: 09
 High quality sequence stop: 661.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3504608"
 /clone_lib="NIH-MGC_21"
 /tissue_type="choriocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 177 a 208 c 224 g 114 t
 ORIGIN

Query Match 22.1%; Score 385; DB 10; Length 723;
 Best Local Similarity 99.6%; Pred. No. 4.2e-166;
 Matches 485; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atgaggaagctcgtgtgtgacacagataaccagcaagatagagagccatgttc 60
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 DB 107 ATGAGGAAGCTGCTGTGGCACAGTAATCCACAGATGATGAGAGGCAATGTTTC 166
 QY 61 ctgaagagcaagaccgaggaagaaacttcctcctcgtgccaagctcatcatcatt 120
 |||||||
 DB 167 CTGAAGGCCAAGACCCGGGAGCAATACCTTTCTCTGTCGTCAGGCTCATTTATTTT 226
 QY 121 cgaagatcataaagaagaalctcaagcttcgcagctgcatatgaatgacatccag 180
 |||||||
 DB 227 CGAGACATTCATTAACAGAAATCTCAAGCTTCCGACAGATGATCTAATGAACACTCCAG 286
 QY 181 agcctgactcgcgagcctcgtcgcgagagcgtgtaattgcatagctcctccgggccc 240
 |||||||
 DB 287 AGCCTGACTGCGGAGACTGCTGCGGAGACCGCTGGAATTGGCATGCTCTCGGGGCGCG 346
 QY 241 ggaagctcctcggggagatgtagcttggtgcatagggagacagcaatgtctctca 300
 |||||||
 DB 347 GGACACTCTCTGGGCGGAGTGGGTAGCCTTTGGTGTGCACGGGACGCAATGTCTCTCA 406
 QY 301 gggcagccgctcctcgggaactcgggagatggccctcacagcatgagctggtctacg 360
 |||||||
 DB 407 GGGCAGCCGCTCTGCGGACCTCGGGGATGGCCCTCACAGATGAGTGTGTGCTACG 466
 QY 361 gcaactccagacccagctcagctcagcagcagtggtgctgcagcagcagcagcag 420
 |||||||
 DB 467 GCAACTCCACAGACCCAGCTGCAAGCAGGAGGCGGCTGCACACACACAGCAACAG 526
 QY 421 cagcagttccagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 480

Db	123	CGAGACATTTATTAACAAGAAATCTCAAGCTTCCGTCAGTGCATGATCTTATGAATGCACTCCAG	182
Qy	181	agcctgactctgaggagacctctgcggagacgcctgtaattgcatgctctccctcgaggccg	240
Db	183	AGCCTGACTGGCGACCTGCTGGGGAGCCGCTGGAAATGGGATGCTCTCCGGGGCCG	242
Qy	241	ggaaagctctggggcgggatggttaacttltgtgtccatgaggacaaatgtctctcca	300
Db	243	GGACAGCTCTGGGCGGGAGGGGTAGCCTTGGTGCATGGGACACCAATGCTCTCTCA	302
Qy	301	gggagagcgctctctggagacctggggagctgagcccccacagatagctgtctgtctacg	360
Db	303	GGGGAGCGGCTCTCTGGGACCTGGGGAGTGGCCCTTCACAGCATGCTGTCTGTACG	362
Qy	361	gcaactccacagaccacagctgcacgtccacagcagatgtgc	398
Db	363	GCACTCCACAGACCAGCTGCAGCTCCAGCAGGTGC	400
RESULT	13		
LOCUS	BE163519/c		
DEFINITION	BE163519	501 bp	mRNA
ACCESSION	BE163519		
VERSION	BE163519.1	GI:8626240	
KEYWORDS	EST		
SOURCE	human		
ORGANISM	Homo sapiens		
			21-JUN-2000
			cdna, mRNA sequence

REFERENCE	TITLE
<p> AUTHORS Eukariyota; Metazoa; Choroidea; Cnaniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 501) Dias Neto, E., Garcia Correa, R., Varjovski-Almeida, S., Briones, M.R. Nagai, M.A., da Silva, W. Jr., Zagzo, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H. Brundstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.U. and Simpson, A.J.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags J. Mol. Biol. 349:1-14 (2000) Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) Contact: Simpson A.J.J.G. </p>	<p> JOURNAL MEDLINE COMMENT </p>

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=tl2-QV3-HT0460-23>)
200-101-P02&ts=2000-02-23&td=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 499.

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FEATURES
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Location/Qualifiers
1..501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="H70460"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning product
derived from OREBES PCR (U.S. Letters Patent applicati
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription o
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
72 a 121 c 192 g 116 t
ORIGIN

```

Query Match	19.5%;	Score 340;	DB 10;	Length 501;
Best Local Similarity	100.0%;	Pred. No. 2e-145;		
Matches 340;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;
QY 735	gcagccacccgatgacagcagccacagctccgcctcccaagctctctccccaagacttga	794		
Db 453	GCAGCCACCGATTCACACAGCCACAGCCTCCGCCCTCCAGGCTCTGCCACGACGTTGA	394		
QY 795	gcagatgcatataaacacagcaccacacacgcgcgcacacaaagccccaagagctccagttgc	854		
Db 393	GCGAGTGCATCACACACACACACACACACCGCACACACAGCCCGACGAGCCTCAAGTGC	334		
QY 855	tcgaacccaaccactcaacaactccgcgcacagctgcgagacccagcctttgtgtcaaggc	914		
Db 333	TCGAACCAACCTCATCACTACTCCGCCACAGTGCAGACCCAGCCTTTGGTGTACAGGC	274		
QY 915	gcaagctctccctctgacaaatgtgttataccacaaccacactgaattttccgagctcc	974		
Db 273	GCAAGCTCTCCCTGGACAATGTTGTATACCCAAACACCACTGTAATTTTCCGAGCTCC	214		
QY 975	gatagttgatgacacacccccccagttccagcccccaagttgacagagacagagacaagtata	1034		
Db 213	GATGTTGTTGCACACACCCCCCATGTGAGCCCCAGTTGACGACGACGACAGCAGCTTACA	154		
QY 1035	gacagctcagagctccacagatgtgtgtctcccgagttccag	1074		
Db 153	GACAGCTCAGGCTGCCACAGTGTGTGCTCCCGAATTCAG	114		

RESULT	14
LOCUS	Bg122694
DEFINITION	Bg122694 956 bp mRNA EST 30-JAN-2001
ACCESSION	6023531822F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4450300 5', mRNA sequence.
VERSION	Bg122694
KEYWORDS	Bg122694.1 GI:12616203
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL	1 (Phases 1 to 956)
COMMENT	NIH-MGC http://mgc.ncl.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.

Email: cgapbos-remail@nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLU at: <http://image.llnl.gov>
 Plate: LHAM10235 row: k column: 05
 High quality sequence stop: 611.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4450300"
 /clone_1lb="NIH_MGC_90"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (Phage-resistant)"
 /note="Organ: liver; Vector: PCMV-SpOrf6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
 246 a 325 c 251 g 134 t

Query Match 18.8%; Score 327; DB 11; Length 956;
 Best Local Similarity 100.0%; Pred. No. 1.9e-139;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1273 agcccaatgacgagcgcgagcccccacagaacttcagtgctccctcaccttgacattaac 1332
 Db 59 AGCCCAATGACGAGC3CGGACCCACAGAACTTCAGTGTCCCTCCACCTGAGACTTTAAAC 118
 QY 1333 aacacgtgtaaaccc2agcctctgtcatlgagccagctggctccagccagagctgagagag 1392
 Db 119 AACACGTGTAAACCC2AGCTCTGTCTATGACCCAGCTGGCTCCAGCCAGAGCTAGGAGCAG 178
 QY 1393 cagtaacctgacaaactgtagagcagctgctgagctacatgagacccctggccagatgac 1452
 Db 179 CAGTACCTGACAA3CTGAAAGCAGCTGTGAGTACATGAGACCCCTGCGCCGCAATGATC 238
 QY 1453 aacaaatgacaaactgagcaagacgaaagaaagacccctgagtaagatgagagcctctg 1512
 Db 239 AACAAATGACAA3AGCAAGACAGAAAGACCTGAGTAAATGAGAGAGCCTTCTG 298
 QY 1513 gacattctgacagaacctctgagagcggtgtccctgaaagaccttgcaaaagtgtgagac 1572
 Db 299 GACATTCTGACAGA3CCCTCGAAGCGGTGTCCCTGAAAGACCTTGCAAAAGTGTGAGATC 358
 QY 1573 gccctggagaacct3aagaatgacatg 1599
 Db 359 GCCCTGGAGAAACT3AAGAAATGACATG 385

RESULT 15
 BG386117 878 bp mRNA EST 12-MAR-2001
 LOCUS 602455292P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:458345 5',
 DEFINITION mRNA sequence:
 BG386117
 ACCESSION BG386117.1 GI:13279563
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euarchonta; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 878)
 AUTHORS NIH-MGC htlp://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished, 1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaib@remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library: Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 Plate: LCM1:07 row: h column: 24
 High quality sequence stop: 742.
 Location/Qualifiers
 1. 878

FEATURES
 SOURCE
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 /clone="IMAGE:458345"
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 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: colon; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 182 a 305 c 240 g 151 t

ORIGIN

Query Match 18.3%; Score 319; DB 11; Length 878;
 Best Local Similarity 99.7%; Pred. No. 8.9e-136;
 Matches 369; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 77 ggaagaaatcccttcctcgtgagcagctcattacatttgaagaaatcataa 136
 Db 2 GGAGAAATCACTTCTCTCGTGCCAGGCTCATATCACTTTTCAGACATTCATAC 61
 QY 137 agaatctcaagcttcgtaagatgatactatgaatgacacccagacccagctgagagc 196
 Db 62 AGAAATCTCAAGCTTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 121
 QY 197 ctgctcgaggaagccgctggaattggcaatgcctccctcgaggccggagacagctctggag 256
 Db 122 CTGCTCGGAGAGCCGCTGGAATGGCAATGCCCTCTCGGGGCGGAGCACTCTTGAGGCG 181
 QY 257 ggaatggtaagcttctgtgcaatggagacaaatgctctcctgaaggacgagccctctg 316
 Db 182 GGATGGGTAGCCTTGTGTCGATGAGAGAGCAATGCTCTCTCAGGGGAGCCGCTCTG 241
 QY 317 ggaactcgaggatggcccccaagacatggctgtgtgtctacgggaactccagaacc 376
 Db 242 GGACCTCGGGATGGCCCTCACAGCATGGCTGTGCTACGGCACTCCACAGACCC 301
 QY 377 agctgacagctcagagagtgagctgcagcagcagcagcagcagcagcagcagcagcagc 436
 Db 302 AGCTGCAGCTCCAGCAGGTGCGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 361
 QY 437 agcagcagcagc 446
 Db 362 AGCAGCAGGC 371

Search completed: April 30, 2002, 20:39:03
 Job time: 14456 sec

Wed May 1 16:36:06 2002

us-09-668-119-1.oli.rst

Page 11

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•
•
•
•

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2002, 17:43:22 ; Search time 92.24 Seconds
(without adjustment)

4272.243 Million cell updates/sec

Title: US-09-668-119-1
1740

Sequence: 1 atgaggaagctgtgtgac.....cacattcggtccagccatga 1740

Scoring table:	OLIGO_NUC	Count
	CGGGG	60

Searched: 351203 seqs, 113238999 residues

Word size : 0

Total number of hits satisfying chosen parameters: 702406

Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

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3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
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5: /cgn2.6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result					Description	
No.	Score	Query	Match	Length	ID	
1	45	2.6	203	4	US-09-043-303-7	Sequence 7, Appli
2	42	2.4	397	3	US-09-253-691-3	Sequence 3, Appli
3	42	2.4	1776	2	US-08-531-9278-1	Sequence 1, Appli
4	42	2.4	1776	4	US-09-041-886-12	Sequence 12, Appli
5	41	2.4	1853	1	US-08-551-110-2	Sequence 2, Appli
6	41	2.4	4279	4	US-09-041-886-22	Sequence 22, Appli
7	38	2.2	1633	3	US-09-234-332-4	Sequence 4, Appli
8	38	2.2	3563	3	US-09-041-886-20	Sequence 20, Appli
9	38	2.2	3596	2	US-08-779-801-5	Sequence 5, Appli
10	38	2.2	3596	4	US-09-298-441-5	Sequence 5, Appli
11	38	2.2	3632	2	US-08-779-801-3	Sequence 3, Appli
12	38	2.2	3632	4	US-09-298-441-3	Sequence 3, Appli
13	37	2.1	228	6	5273901-10	Patent No. 5273901
14	37	2.1	5482709-9		Patent No. 5482709	
15	37	2.1	286	2	US-08-332-766A-6	Sequence 6, Appli
16	37	2.1	510	2	US-08-134-009-150	Sequence 150, Appli
17	37	2.1	510	2	US-08-458-356-150	Sequence 150, Appli
18	37	2.1	510	4	US-08-460-736-150	Sequence 3, Appli
19	37	2.1	1332	2	US-08-481-814A-3	Sequence 1, Appli
20	37	2.1	1489	3	US-08-836-582-1	Sequence 1, Appli
21	37	2.1	1489	4	US-09-285-566-1	Sequence 13, Appli
22	37	2.1	2770	4	US-09-008-657A-13	Sequence 13, Appli
23	36	2.1	51	1	US-08-068-747-1	Sequence 1, Appli
24	36	2.1	69	4	US-09-043-303-13	Sequence 13, Appli
25	36	2.1	78	4	US-09-043-303-13	Sequence 12, Appli
26	36	2.1	154	1	US-08-469-802B-6	Sequence 6, Appli
27	36	2.1	154	2	US-08-267-803B-6	Sequence 6, Appli

28	36	2.1	165	4	US-09-04-303-17	Sequence 17, Appl
29	36	2.1	168	1	US-08-469-802B-3	Sequence 4, Appl
30	36	2.1	168	2	US-08-267-803B-4	Sequence 4, Appl
31	36	2.1	171	1	US-08-469-802B-5	Sequence 5, Appl
32	36	2.1	171	2	US-08-267-803B-5	Sequence 5, Appl
33	36	2.1	195	1	US-08-469-802B-2	Sequence 2, Appl
34	36	2.1	195	2	US-08-267-803B-2	Sequence 2, Appl
35	36	2.1	234	1	US-08-469-802B-3	Sequence 3, Appl
36	36	2.1	234	2	US-08-267-803B-3	Sequence 3, Appl
37	36	2.1	300	4	US-09-135-921B-3	Sequence 3, Appl
38	36	2.1	335	2	US-08-531-927B-3	Sequence 3, Appl
39	36	2.1	477	4	US-09-135-994-1	Sequence 1, Appl
40	36	2.1	506	1	US-08-469-802B-7	Sequence 7, Appl
41	36	2.1	506	2	US-08-267-803B-7	Sequence 7, Appl
42	36	2.1	688	4	US-08-998-416-915	Sequence 915, Appl
43	36	2.1	715	4	US-08-998-416-590	Sequence 590, Appl
44	36	2.1	1080	2	US-08-918-727-2	Sequence 2, Appl
45	36	2.1	1080	3	US-09-205-680A-2	Sequence 2, Appl

ALIGNMENTS

[illegible]


```

FEATURE: NAME/KEY: CDS
; LOCATION: 239..3794
; US-09-041-886-22

Query Match          2.4%; Score 41; DB 4; Length 4279;
Best Local Similarity 100.0%; Pred. No. 1.4e+09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 664 caacagcacagcagcagcagcagcagcagcagcagca 704
      |||||||
Db 1691 CAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCA 1731

RESULT 7
US-09-234-332-4
; Sequence 4, Application US/09234332A
; Patent No. 6067168
GENERAL INFORMATION:
APPLICANT: Cedars-Sinai Medical Center
APPLICANT: Michel F. Levesque, M.D.
APPLICANT: Toomas Neuman, Ph.D.
TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO
TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS
FILE REFERENCE: P07 41494
CURRENT APPLICATION NUMBER: US/09/234.332A
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1635
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: gene
LOCATION: (0)..(0)
OTHER INFORMATION: Achaete scute homologous protein (ASH1) gene;
US-09-234-332-4

Query Match          2.2%; Score 38; DB 3; Length 1635;
Best Local Similarity 100.0%; Pred. No. 3.2e+08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 cagcagcagcagcagcagcagcagcagcagcagcg 710
      |||||||
Db 589 cagcagcagcagcagcagcagcagcagcagcagcg 626

RESULT 8
US-09-041-886-20
; Sequence 20, Application US/09041886
; Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabinzadeh, Sharrooz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 3563 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 3..3556
US-09-041-886-20

Query Match 2.2%; Score 38; DB 4; Length 3563;
Best Local Similarity 100.0%; Pred No. 3.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 cagcagcagcagcagcagcagcagcagcagcagc 710
|||||
DB 2970 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3007

RESULT 9
US-08-779-801-5
Sequence 5, Application US/08779801
Patent No. 5853995
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of
TITLE OF INVENTION: Large Scale Genotyping of
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,801
FILING DATE: January 7, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3596
TYPE: nucleic acid
STRANDEDNESS: double-stranded

TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
TISSUE TYPE: human
IMMEDIATE SOURCE: brain
LIBRARY: primary human brain cDNA
CLONING: B1(V2)-GGCAG
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
US-08-779-801-5

Query Match 2.2%; Score 38; DB 2; Length 3596;
Best Local Similarity 100.0%; Pred No. 3.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 673 cagcagcagcagcagcagcagcagcagcagcagc 710
|||||
DB 2970 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3007

RESULT 10
US-09-298-441-5
Sequence 5, Application US/09298441
Patent No. 609307
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of Diseases
TITLE OF INVENTION: Large Scale Genotyping of Diseases
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCreight & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,441
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,273
FILING DATE: June 8, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968D/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3596 basepairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: cDNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:

ORGANISM: human
TISSUE TYPE: brain
IMMEDIATE SOURCE:
LIBRARY: Primary human brain cDNA
CLONE: BI-1(V2)-GGCAG
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
FEATURE:
US-09-298-441-5

Query Match 2.2%; Score 38; DB 4; Length 3596;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 673 cagcagcagcagcagcagcagcagcagcagcagc 710
|||||
Db 2970 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3007

RESULT 11
US-08-779-801-3
Sequence 3, Application US/08779801
Patent No. 5853995
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of
Diseases and a Diagnostic Test for Spinocerebellar Ataxia Type
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,801
FILING DATE: January 7, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3632
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA
HYPOTHEICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FRAGMENT TYPE:
ORGANISM: human
TISSUE TYPE: brain
IMMEDIATE SOURCE:
LIBRARY: Primary human brain cDNA
CLONE: BI-1-GGCAG
POSITION IN GENOME:

CHROMOSOME/SEGMENT: 19p13
US-08-779-801-3

Query Match 2.2%; Score 38; DB 2; Length 3632;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 673 cagcagcagcagcagcagcagcagcagcagcagc 710
|||||
Db 3006 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3043

RESULT 12
US-09-298-441-3
Sequence 3, Application US/09298441
Patent No. 6303307
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
TITLE OF INVENTION: Large Scale Genotyping of Diseases
and a Diagnostic Test for Spinocerebellar Ataxia Type 6
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,441
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/093,273
FILING DATE: June 8, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5968D/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3632 basepairs
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: cDNA
HYPOTHEICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: brain
IMMEDIATE SOURCE:
LIBRARY: Primary human brain cDNA
CLONE: BI-1-GGCAG
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 19p13
US-09-298-441-3

Query Match 2.2%; Score 38; DB 4; Length 3632;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 673 cagcagcagcagcagcagcagcagcagcagcagc 710
|||||
Db 3006 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3043

RESULT 13
5273901-10
PATENT NO. 5273901
APPLICANT: JACOBSON, JAMES W.; STRAUSSBERG, ROBERT L.; WILSON,
SUSAN D.; POPE, SHARON H.; STRAUSSBERG, SUSAN L.; RUFF, MICHAEL D.;
AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS
SPOROZOITE 21.5 KB ANTIGEN, AC-6B
NUMBER OF SEQUENCES 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/581,693
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1988
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
SEQ ID NO: 10
5273901-10
LENGTH: 228

Query Match 2.1%; Score 37; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 673 cagcagcagcagcagcagcagcagcagcagcagc 709
|||||
Db 181 cagcagcagcagcagcagcagcagcagcagcagc 217

RESULT 14
5482709-9
PATENT NO. 5482709
APPLICANT: JACOBSON, JAMES W.; STRAUSSBERG, ROBERT L.; WILSON,
SUSAN D.; POPE, SHARON H.; STRAUSSBERG, SUSAN L.; RUFF, MICHAEL D.;
AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.
TITLE OF INVENTION: EIMERIA ANTIGENIC COMPOSITION WHICH
ELICITS ANTIBODIES AGAINST AVIAN COCCIDIOSIS
NUMBER OF SEQUENCES 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,432
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 581,693
FILING DATE: 12-SEP-1990
APPLICATION NUMBER: 215,162
FILING DATE: 05-JUL-1989
APPLICATION NUMBER: 746,520
FILING DATE: 19-JUN-1985
APPLICATION NUMBER: 627,811
FILING DATE: 05-JUL-1984
SEQ ID NO: 9
5482709-9
LENGTH: 228

Query Match 2.1%; Score 37; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 673 cagcagcagcagcagcagcagcagcagcagcagc 709
|||||
Db 181 cagcagcagcagcagcagcagcagcagcagcagc 217

RESULT 15
US-08-332-766A-6
Sequence 6, Application US/08332766A
PATENT NO. 5843647
GENERAL INFORMATION:
APPLICANT: JEFFREYS, Alec J.
APPLICANT: ARMOUR, John
TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/CB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-766A-6

Query Match 2.1%; Score 37; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 673 cagcagcagcagcagcagcagcagcagcagcagc 709
|||||
Db 187 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 223

Search completed: April 30, 2002, 20:40:57
Job time: 10655 sec

Wed May 1 16:36:05 2002

us-09-668-119-1.011.rml

1
2
3
4
5

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2002, 16:13:27 ; Search time 1517.62 Seconds
(without alignments)
12320.380 Million cell updates/sec

Title: US-09-668-119-1

Perfect score: 1740

Sequence: 1 atgaggaagctgtgtgtgc.....cacatcttcacgatga 1740

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372893281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estipl:*
6: em_estlba:*
7: em_estro:*
8: em_estov:*
9: em_hlc:*
10: qb_estl:*
11: qb_estl2:*
12: qb_hlc:*
13: qb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	722.8	41.5	776	11	BG750043 602703874
2	697.6	40.1	730	11	BG766214 602737942
3	662	38.0	2752	12	BC005027 Homo sapi
4	655	37.6	886	11	BG281923 602403104
5	650.8	37.4	757	10	AL046886 DKFZP586E
6	615.2	35.4	620	10	BE384305 601272684
7	572.8	32.9	939	11	BC336790 602405533
8	536.6	30.8	723	10	BE279307 601157640
9	530	30.5	1019	11	BE335275 602403789
10	527	30.3	914	11	BG468341 602509947
11	526.8	30.3	656	10	BE390284 601285167
12	524.4	30.1	526	10	BE019568 ba83f05.y

Result	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	BG750043	602708813F1 NIH_MGC_43	BG750043	1	776 bp mRNA	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
13	512.8	29.5	756	11	BG746380	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
14	480.4	27.6	482	10	AA664125	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
15	469.4	27.0	524	10	BE410770	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
16	469.2	27.0	733	10	BE391135	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
17	459.8	26.4	498	10	AW603679	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
18	453	26.0	942	11	BG338685	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
19	443.2	25.5	956	11	BG122694	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
20	428.8	24.6	1157	11	BG177319	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
21	401.6	23.1	1864	12	BC003221	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
22	398.2	22.9	876	11	BC386117	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
23	366.2	22.8	795	11	BG915202	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
24	386	22.2	401	10	BE163519	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
25	383.2	22.0	543	11	BI024741	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
26	375	21.7	594	10	BE284329	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
27	377	21.6	557	11	BG421322	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
28	358.2	20.6	486	10	AW747905	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
29	348.2	20.0	568	11	BI089323	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
30	343.8	19.8	690	10	BE251464	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
31	325.8	18.7	543	10	AW227792	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
32	323.8	18.6	386	11	BG982761	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
33	320.4	18.4	386	11	BG982754	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
34	310.2	17.8	416	11	BI015868	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
35	310	17.8	514	10	AT187536	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
36	307.8	17.7	487	11	BF600990	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
37	303	17.4	313	11	N49344	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
38	303	17.4	367	10	AA982166	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
39	301.6	17.3	335	11	BI011820	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
40	297.6	17.1	382	11	BG962938	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
41	295.4	17.0	1107	11	BF143909	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
42	283.4	16.3	424	10	AW501171	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
43	278.4	16.0	428	11	BE889171	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
44	278.2	16.0	435	11	BF922390	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov
45	273	15.7	810	11	BG686794	EST	Homo sapiens	NIH-MGC	http://mgc.nci.nih.gov/	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov

ALIGNMENTS

FEATURES
source

High quality sequence stop: 743.
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QY	1223	ccccatctccagbaggcttctctgcccagccccttaacgcgcagccctccagagcccaatgta	1282
Db	422	CCCCAATCTCCCAAGTAGCTTCTGTGCCACAGCCCTCTACCGCAGCCCTCCAGAACCCAGTGA	481
QY	1283	cgagcgagagccccaagaactcagtgctccctcaacttgagaccttlaaacacactgtga	1342
Db	482	CGGCGGGGAGCCCAAGAACTTCAGTGTCCCTTACTGTGACCTTTAAACACACTGTGA	541
QY	1343	accocagctctgcatgagcccaagtgtgtccacagcgtctgagagcaagcagtaactgtg	1402
Db	542	ACCCGAGCTCTGTCTCATGTAGCCAGCTGGCTTCAACCCAGGCTGAGGAGCAGTAGTACTGG	601
QY	1403	acaaagctggaagaagctgtcgaagtaactcgaagccctcgagccgcatagatcaacaagaatcg	1462
Db	602	ACAAAGCTGAAGAAGCTGTGGAATGATCATCGAGCCCTCTGCCCTCAATGATTAACAAAGATGG	661
QY	1463	acaaagaa-cgaagacaga-aaaagaagactgagtaagatlaaagaagctctggaacttct	1520
Db	662	ACAAAGAACGAAAGACAGACACAAAGAGAACTGATTAAGATCAAGAGCTTCTGGACATTCT	721
QY	1521	gaacagacc 1528	
Db	722	GACAGAAC 729	

RESULT	3		
LOCUS	BC005027		
DEFINITION	BC005027	2752 bp	mRNA
ACCESSION	BC005027		HTC
VERSION	BC005027.1		12-JUL-2001
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		

REFERENCE	1 (bases 1 to 2752)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (26-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

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1	1080	1139	+	LOCUS	ccagagcagcctccccaatgtgtctctgcgttcacccgggccaagatgtcgaaccgcga	1139
1	716	775	+	LOCUS	ccagagcagcctccccaatgtgtctctgcgttcacccgggccaagatgtcgaaccgcga	775
1	1140	1199	+	LOCUS	gtcgatgccccctccccccagcgtgccccggagccgggccaagcccacatcaaacccaa	1199
1	776	835	+	LOCUS	gtcgatgccccctccccccagcgtgccccggagccgggccaagcccacatcaaacccaa	835
1	1200	1259	+	LOCUS	ctccaacgttcagctcttgcccttgcccaatctcccaatgactctctctgcccagcccccaac	1259
1	836	895	+	LOCUS	ctccaacgttcagctcttgcccttgcccaatctcccaatgactctctctgcccagcccccaac	895
1	1260	1319	+	LOCUS	gcagcctccccaagagcccaatgtgaagcgcgcgagaccccaagaactcagtgctccctaac	1319
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1	1380	1439	+	LOCUS	ggtctgagagcagcagcagtaacttgacaaagctgaagcagctgttcgaatgatactgaagccct	1439
1	1016	1075	+	LOCUS	ggtctgagagcagcagcagtaacttgacaaagctgaagcagctgttcgaatgatactgaagccct	1075
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DEFINITION	BG281923	886 bp	mRNA	EST
ACCESSION	602403104F1	NIH_MGC_20	Homo sapiens	CDNA clone IMAGE:4545433 5',
			mRNA	sequence.
	BG281923			

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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FEATURES

Source

BASE COUNT	ORIGIN
234 a	299 c
231 g	122 t

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Best Local Similarity	93.7%	Pred. No. 1.7e-96		
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Db 2	gtctctctcagcagccaccctctctctggagaccctcggggagatggccctctacagcatgctgt	61		
QY 351	cgtgcttacggcaaatccacacagaccagctgagcttcacagagtggtgcctctgcagcaga	410		
Db 62	cggtgtacggcaaatctccacagaccagctgagcttcacagagtggtgcctctgcagcaga	121		
QY 411	ggagcaacagcagcagcttcacagcagcagcagcagcagcagcagcagcagcagcaga	470		
Db 122	ggagcaacagcagcagcttcacagcagcagcagcagcagcagcagcagcagcagcaga	181		
QY 471	ggagcaacagcagcagcttcacagctccagcagagtgatgcatgtcagcagcagctccaagcag	530		
Db 182	ggagcaacagcagcagcttcacagctccagcagagtgatgcatgtcagcagcagctccaagcag	241		
QY 531	agtgccagcagcagcagcttcacagctccagcagcagcagcagcagcagcagcagcagcagc	590		
Db 242	agtgccagcagcagcagcttcacagctccagcagcagcagcagcagcagcagcagcagcagc	301		
QY 591	gcatcctcaaatctcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	650		
Db 302	gcattcattcaaaatctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	361		
QY 651	gctgcagcctcccaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	706		
Db 362	gctgcagcctcccaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	421		
QY 707	aggctcttgagagccatagccaccaattcagcagcagcagcagcagcagcagcagcagcagc	765		

Db 422 GGCCTTTCGAGAGGCCACGCCACCAATTTCACGCCACGCCACCCATTGCAGCAGCCACAGCTCCG 481

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Db 781 TCCCGGAATTCAGATGATATC 799

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VERSION	DKEP586E217.5,		mRNA sequence.
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SOURCE	human.		
ORGANISM	Homo sapiens		

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VERSION        BG468341.1 (1:13400611)
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ORGANISM       Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 914)
AUTHORS       NIH-MGC http://mgi.nci.nih.gov/
TITLES        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cga@r-email.nih.gov
                Tissue Procurement: ATCC
                CDNA Library Preparation: Ling Hong/Rubin Laboratory
                DNA Sequencing by: NIH Intramural Sequencing Center
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
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                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
                (Stratagene) and Superscript II RT (Life Technologies)."
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DB 3 CAACGTCACTCTG03CCCTCCCACTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 62
QY 1263 gccctccacagacccagtgacgagcgagacccacagaaactcagtgctccctcacctg 1322
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DB 63 GCCCTCCCAAGGCCAGTGAAGGGGGGAGCCCAACAACTTCAGTGTCCCTCACCTGG 122
QY 1323 accttaaacacaccttgtaaccacagctctgcatgagccagctgctgctccacagc 1382
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DB 123 ACCTTTAAACACACCTGTGAACCCCACTCTGTCAATGAGCCCACTGCTCCACGACG 182
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DB 183 TGAAGACAGACAGTACTGTGAAGAGCCCTCGAAGCGGTGTCCCTGAAGACCTTGCAAAA 242
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ACCESSION    BE390284
VERSION      BE390284.1 GI:9335562
KEYWORDS
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 656)
AUTHORS       NIH-MGC http://mgi.nci.nih.gov/
TITLES        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cga@r-email.nih.gov
                Tissue Procurement: ATCC
                CDNA Library Preparation: Ling Hong/Rubin Laboratory
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: L1CM257 row: e column: 18
                High quality sequence stop: 588.
                Location/Qualifiers
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                EcoRI; CDNA made by oligo-dt priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Library constructed by Ling Hong
                in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
                (Stratagene) and Superscript II RT (Life Technologies)."
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Matches 613; Conservative 0; Mismatches 32; Indels 7; Gaps 6:
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    |||
DB 1 CAGCGGCGACAGCTCTCAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 60
QY 598 caaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 657
    |||
DB 61 CAAATTCAGCAACATATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
QY 658 ctccaacaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 717
    |||
DB 121 CTCCAACAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 180
QY 718 gccacagcaccacattcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 777

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2907009"
/clone_lib="NH_MGC_21"
/tissue_type="Choriocarcinoma"
/lab_host="DH010 (phage-resistant)"
/notes="Organ: placenta; Vector: pORF7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGCAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University

```

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA library Preparation: Ling Hong/Rubin Laboratory
CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
plate: LLCMI708 row: p column: 12

High quality sequence stop: 756.
location/Qualifiers

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4857083"
/clone_1lb="NIH-MGC-15"
/tissue-type="adenocarcinoma cell line"
/lab-host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pORF7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 179 a 264 c 186 g 126 t
others

ORIGIN

Query Match 29.5%; Score 512.8; DB 11; Length 756;
Best Local Similarity 99.4%; Pred. No. 4.2e-75;
Matches 525; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1214 ctggcctgctgcccctccctccagtagcttctgcccagccctccagccagccctccagc 1273
1215 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
9 CAGGCCAGGCCCA TCTCCAGTAGTCTCTGCCACGCCCTCCAGCCAGCCCTCCAG 68
1274 gccagtgagcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc 1333
1275 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 GCCCAGTGAGCGGCGGCAACCCACAGAACTTCACTGCTCCCTCAGCCGACCTTTAAAC 128
1334 cactctgtgaaacccctgctctgctgctgctgctgctgctgctgctgctgctgctgctg 1393
1335 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
129 CACTGTGAAACCCAGCTCTGTCTAGAGCCAGCTGCTCCAGCCAGCTGAGAGAGAGC 188
1394 agtacttgacaagctgaaagcagctgtcgaagtaacatcgaagccctgagcagatgac 1453
1395 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 AGTACCTGGACAAAGCTGACAGCTGTGCAAGTACATGAGCCCTCCGCGCATATCA 248
1454 acaagatcgacaagctgaaagcagaaagaaagcagctgaaatgaatgaagcctctg 1513
1455 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
249 ACAAGATCGACAAAGTACCAAGACAGAAAGAACCTGAGTAAGTAAGAAAGAGCTTCTG 308
1514 acattctgacaagcctctcgaagcgtgtccctgaaagcctctgcaaaatgtgaaatcg 1573
1515 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
309 ACATTCTGACAGAC TCTCCAGAGGCTGCTCCCTGAAAGACCTTGCAAAAGTGTGAGATCG 368
1574 cctctggaagaaatcagaatgact-gcggctgcccactcccccagcccccagctgcccac 1632
1575 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
369 CCCCGAGAAACTCMAAATGACATGCGGTGCGCACTCCGCCACGCCGCCCGGTGCGAC 428
1633 cgaccagaagcagctcctcgaagcgtgtccctgaaagcctctgcaaaatgtgaaatcg 1692
1634 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
429 CGACCAACACACAGTACTTATGCGAGCCCTCTGCAATGCGTCTGCGCAACATCGCT 488
1693 cactctgtcctcaacattccctgttaccgcaatcgttccagcagatga 1740
1694 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
489 CACTGTCTTCAACCAATTCCTGTACCGCACTTCTGTTCCAGGCATCA 536

RESULT 14
AA664125/c 482 bp mRNA EST 12-NOV-1997
LOCUS AA664125
DEFINITION ac06c04.s1 StrataGene lung (#937210) Homo sapiens cDNA clone
IMAGE:855654 3' similar to contains element MSRI MSRI repetitive
element; mRNA sequence.
ACCESSION AA664125
VERSION AA664125.1 31:2618116
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 482)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
Kizman, D., Kucuba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
White, Y., Wylie, T., Waterston, R., and Wilson, R.

TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Wilson R.
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 425.

FEATURES

source

1..482
/organism="Homo sapiens"
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/sex="male"
/dev-stage="72 years"
/lab-host="SOLR cells (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site:1: EcoRI
; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo
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Vector: -5' adaptor sequence: 5' GAATTCGGACGAG 3' -3'
adaptor sequence: 5' CTCGACCTTTTCTTTTCTTTT 3' "

location/Qualifiers

BASE COUNT 51 a 113 c 176 g 142 t
ORIGIN

Query Match 27.6%; Score 480.4; DB 10; Length 482;
Best Local Similarity 99.8%; Pred. No. 8.9e-70;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

428 tccacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 487
429 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
482 TCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 423
488 tccagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 547
489 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
422 TCCAGCCTCAGCAGAGTGCATGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 363
548 agctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 607
549 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
362 AGCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 303
608 aacacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 667
609 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
302 AACACATACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 243
668 agcaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 727
669 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
242 AGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 183
728 caattcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 787
729 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
182 CAATTTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 123
788 agctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 847
789 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
122 ACTTCAGC 63
848 cagttgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 907
849 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
62 CAGTTGTGAGAACCAACATCAGCAACTCCGCGCACAGTCCAGAGCCAGGCTTTGGGT 3

QY	908	ca	909
Db	2	CA	1

RESULT	15
BEA10770/c	
LOCUS	524 bp mRNA
DEFINITION	BEA10770 601016611f NH_MGC_21 Homo sapiens cDNA clone IMAGE:3636021 5'

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 524)
NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at: image.llnl.gov
Plate: LINC333 row: b column: 22
High quality sequence start: 48
High quality sequence stop: 522.
Location/Qualifiers

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/organism="Homo sapiens"
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/clone="IMAGE:3636021"
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/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; site_1: XhoI;
site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAcGAg(g). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT
65 a 125 c 204 g 130 t

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Query Match	27.0%;	Score 469.4;	DB 10;	Length 524;
Best Local Similarity	94.8%;	Pred. No. 5.7e-68;		
Matches 496; Conservative	0;	Mismatches 26;	Indels 1;	Gaps 1

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Db	524	GCAGGGATATGACACAGCTGCAAGCTCCCAACACAGCAACGACGACGACGACGACGACGA	4655
QY	696	gaagcagcagcagcagcgttctgtgagagcccaagcccaatctcaagcccaacgagatgcagcagcc	7555
Db	464	GCAGGACGACGACGAGCTTTGTCAGGCGCCGACGACCAATTCAGGCGCCAGCCAGTGCAGGACCC	4050
QY	756	gaagcctcgcgcctctcccaagagctctgcccacagacgctgcagacagatgatatacaacaagca	8155
Db	404	ACAGGCTCGCGCCTTCCAGGCTCTGCCCCGACGAGCTGCGAGCGAGTCATCACACACAGCA	3455
QY	816	ccaccagcgcgcacacacaagcccccaagacgctccagatctgtctcaagaaaccaatcaacaact	8757
Db	344	CCACCAGCGCGACACACAGCGCCCGACGAGCCTTCAGTTGGTCGAAACCAACATCAACAAC	2855
QY	876	ccccgcacagctcgcagagcccaagccttctgtgtctcaacagcgcgcagcgtctctcccttgacaat	9355

Search completed: February 28, 2002, 18:34:06
Job time: 8439 sec

D _b	284	CCCCGACAGTCCGACGAGCACCCTTTGGTGTCACAGCGCCAAAGCTCTCCCTTGACCAAT	225
Q _y	936	gttataaccacaacacacactggaattttgcagagctccgaatagtgttgtaagaagccc-	994
D _b	224	GTTGTATTATCCCAACACACACTGMAATTTTGTCCGAGCTCCGATGTGTGTGCAGAGCCAC	165
Q _y	995	cagttcagccccaggtgtcaagaacagcacagacagtagtaeagacagctcaggttcaccaga	105
D _b	164	CAGTGCAGCCCCAGTGCAGACGACGACGACACACAGTACAGACAGCTTCAGGCCAATA	105
Q _y	1055	tgtgtgtcccccaggtcaggtcaggtcagccacagagcagcctcccacgctgtctctgcgctaac	111
D _b	104	TGTGTGCTCCCGAGTCCAGGTACGACGTACGCCAGACGCTCCCATGTGHTCTCGCGCTAC	45
Q _y	1115	cggagccagcaggttgtcaaccgcccgagtcgatgtgcctccctccccc	1157
D _b	44	GGGGCCACGACGACACAGACCTTMACCAAGCTTAAGTGGCCCC	2

Fri Mar 1 09:12:00 2002

us-09-668-119-1.rst

Page 12